

SEQUENCE LISTING

<110> Tsuchiya, Masayuki
Saito, Mikiyoshi
Ohtomo, Toshihiko

<120> NOVEL METHOD FOR GENE CLONING

<130> 06501-070001

<140> US 09/700,820

<141> 2000-11-20

<150> PCT/JP99/02341

<151> 1999-04-30

<150> JP 10/138652

<151> 1998-05-20

<150> JP 10/279876

<151> 1998-10-01

<160> 39

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Peptide Linker Sequence

<400> 1

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 2

<211> 1035

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1035)

<400> 2

atg ctg gcc gtc ggc tgc gcg ctg ctg gct gcc ctg ctg gcc gcg ccg 48
Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro
1 5 10 15

gga gcg gcg ctg gcc cca agg cgc tgc cct gcg cag gag gtg gca aga 96
Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
20 25 30

ggc gtg ctg acc agt ctg cca gga gac agc gtg act ctg acc tgc ccg 144
Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
35 40 45

ggg gta gag ccg gaa gac aat gcc act gtt cac tgg gtg ctc agg aag	192
Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys	
50 55 60	
ccg gct gca ggc tcc cac ccc agc aga tgg gct ggc atg gga agg agg	240
Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg	
65 70 75 80	
ctg ctg ctg agg tcc gtg cag ctc cac gac tct gga aac tat tca tgc	288
Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys	
85 90 95	
tac cgg gcc ggc cgc cca gct ggg act gtg cac ttg ctg gtg gat gtt	336
Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val	
100 105 110	
ccc ccc gag gag ccc cag ctc tcc tgc ttc cgg aag agc ccc ctc agc	384
Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser	
115 120 125	
aat gtt gtt tgt gag tgg ggt cct cgg agc acc cca tcc ctg acg aca	432
Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr	
130 135 140	
aag gct gtg ctc ttg gtg agg aag ttt cag aac agt ccg gcc gaa gac	480
Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp	
145 150 155 160	
ttc cag gag ccg tgc cag tat tcc cag gag tcc cag aag ttc tcc tgc	528
Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys	
165 170 175	
cag tta gca gtc ccg gag gga gac agc tct ttc tac ata gtg tcc atg	576
Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met	
180 185 190	
tgc gtc gcc agt agt gtc ggg agc aag ttc agc aaa act caa acc ttt	624
Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe	
195 200 205	
cag ggt tgt gga atc ttg cag cct gat ccg cct gcc aac atc aca gtc	672
Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val	
210 215 220	
act gcc gtg gcc aga aac ccc cgc tgg ctc agt gtc acc tgg caa gac	720
Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp	
225 230 235 240	
ccc cac tcc tgg aac tca tct ttc tac aga cta cgg ttt gag ctc aga	768
Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg	
245 250 255	
tat cgg gct gaa cgg tca aag aca ttc aca aca tgg atg gtc aag gac	816
Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp	
260 265 270	

ctc cag cat cac tgt gtc atc cac gac gcc tgg agc ggc ctg agg cac 864
 Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
 275 280 285

gtg gtg cag ctt cgt gcc cag gag gag ttc ggg caa ggc gag tgg agc 912
 Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
 290 295 300

gag tgg agc ccg gag gcc atg ggc acg cct tgg aca gaa tcc agg agt 960
 Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
 305 310 315 320

cct cca gct gag aac gag gtg tcc acc ccc atg cag gca ctt act act 1008
 Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr
 325 330 335

aat aaa gac gat gat aat att ctc ttc 1035
 Asn Lys Asp Asp Asp Asn Ile Leu Phe
 340 345

<210> 3
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "IL6R1", an artificially synthesized primer sequence

<400> 3
 ttccaattcc caccatgctg gccgtcggct gcgcgctgct 40

<210> 4
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "IL6R2", an artificially synthesized primer sequence

<400> 4
 ttccaattcg aagagaatat tatcatcgtc tttatt 36

<210> 5
 <211> 768
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(768)

<220>
 <223> Description of Artificial Sequence: a designed single chain Fv gene sequence

<400> 5

cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga cct agc cag	48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln	
1 5 10 15	
acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att acc agc gat	96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp	
20 25 30	
cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt ctt gag tgg	144
His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp	
35 40 45	
att gga tac att agt tat agt gga atc aca acc tat aat cca tct ctc	192
Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu	
50 55 60	
aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac cag ttc agc	240
Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser	
65 70 75 80	
ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt tat tat tgt	288
Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gca aga tcc cta gct cgg act acg gct atg gac tac tgg ggt caa ggc	336
Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly	
100 105 110	
agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt ggt ggt ggt	384
Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
115 120 125	
tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc cca agc agc	432
Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
130 135 140	
ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aga gcc agc	480
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser	
145 150 155 160	
cag gac atc agc agt tac ctg aat tgg tac cag cag aag cca gga aag	528
Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys	
165 170 175	
gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac tct ggt gtg	576
Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val	
180 185 190	
cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc	624
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr	
195 200 205	
atc agc agc ctc cag cca gag gac atc gct acc tac tac tgc caa cag	672
Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln	
210 215 220	

ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag gtg gaa atc 720
 Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 225 230 235 240

aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat 768
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 245 250 255

<210> 6
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "TMT1", an artificially synthesized primer sequence

<400> 6
 ggtgtcgcact ccaggtcca actgcaggag ag 32

<210> 7
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "LINK1", an artificially synthesized primer sequence

<400> 7
 ctgcgtcacag tctctcagg tgggtggtggt tc 32

<210> 8
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "LINK3", an artificially synthesized primer sequence

<400> 8
 gacatccaga tgaccagag cccaagcagc ctgagcgc 38

<210> 9
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "SCP-C", an artificially synthesized primer sequence

<400> 9
 gctgaattct tattatttat cgtcatcgtc tttgtagtca agcttatcag atggcgggaa 60

gat 63

<210> 10
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FLAG peptide

<400> 10
 Met Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 11
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "LINK2", an artificially synthesized primer sequence

<400> 11
 aaccaccacc acctgaggag actgtgacga ggct 34

<210> 12
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "LINK4", an artificially synthesized primer sequence

<400> 12
 aggctgcttg ggctctgggt catctggatg tccga 35

<210> 13
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "TMT2", an artificially synthesized primer sequence

<400> 13
 atccgcggcc gcttattatt tatcgtcacg gtcttt 36

<210> 14
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: leader sequence
 <400> 14

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val Asp Ser

<210> 15
 <211> 106
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "S-FLAG1", an artificially synthesized oligonucleotide sequence

<400> 15
 aattcccacc atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt 60
 cgactccgac tacaagacg atgacgataa aggtaccgcg gccgcg 106

<210> 16
 <211> 106
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "S-FLAG2", an artificially synthesized oligonucleotide sequence

<400> 16
 gatccgcggc cgcggtacct ttatcgatcat cgtctttgta gtcggagtcg acacctgtag 60
 ctgttgctac caagaagagg atgatacagc tccatcccat ggtggg 106

<210> 17
 <211> 2995
 <212> DNA
 <213> Mus musculus

<220>

<221> CDS

<222> (29)..(2839)

<400> 17
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 ttctgtatgt tgggaacatc cctgcaag atg tca gca cca agg att tgg cta 112
 Met Ser Ala Pro Arg Ile Trp Leu
 1 5

gcg caa gct ttg ctt ttt ttc ctc acc act gaa tct ata ggt caa ctt 160
 Ala Gln Ala Leu Leu Phe Phe Leu Thr Thr Glu Ser Ile Gly Gln Leu
 10 15 20

ttg gaa ccg tgt ggt tac atc tac cct gaa ttt cca gtt gtc cag cgc 208
 Leu Glu Pro Cys Gly Tyr Ile Tyr Pro Glu Phe Pro Val Val Gln Arg
 25 30 35 40

ggc tgc aac ttc act gcc att tgt gtg ctg aag gag gcg tgt ctg cag	256
Gly Ser Asn Phe Thr Ala Ile Cys Val Leu Lys Glu Ala Cys Leu Gln	
45 50 55	
cat tac tac gtg aat gcc agc tac atc gtg tgg aag acc aac cat gct	304
His Tyr Tyr Val Asn Ala Ser Tyr Ile Val Trp Lys Thr Asn His Ala	
60 65 70	
gct gtt ccc agg gag cag gtc act gtc atc aac aga acc acg tcc agt	352
Ala Val Pro Arg Glu Gln Val Thr Val Ile Asn Arg Thr Thr Ser Ser	
75 80 85	
gtc acg ttc aca gac gtg gtc ctc ccg agc gtg cag ctc acc tgc aac	400
Val Thr Phe Thr Asp Val Val Leu Pro Ser Val Gln Leu Thr Cys Asn	
90 95 100	
atc ctg tcc ttt ggg cag atc gag cag aat gtg tat gga gtc acc atg	448
Ile Leu Ser Phe Gly Gln Ile Glu Gln Asn Val Tyr Gly Val Thr Met	
105 110 115 120	
ctt tca ggc ttt cct cca gat aaa cct aca aat ttg act tgc att gtg	496
Leu Ser Gly Phe Pro Pro Asp Lys Pro Thr Asn Leu Thr Cys Ile Val	
125 130 135	
aat gag ggg aag aat atg ctg tgc cag tgg gac ccc gga agg gag act	544
Asn Glu Gly Lys Asn Met Leu Cys Gln Trp Asp Pro Gly Arg Glu Thr	
140 145 150	
tac ctt gaa aca aac tac act ttg aaa tca gag tgg gca aca gag aag	592
Tyr Leu Glu Thr Asn Tyr Thr Leu Lys Ser Glu Trp Ala Thr Glu Lys	
155 160 165	
ttt cct gat tgc cag tca aag cat ggc act tca tgt atg gtc agc tac	640
Phe Pro Asp Cys Gln Ser Lys His Gly Thr Ser Cys Met Val Ser Tyr	
170 175 180	
atg ccc acc tat tat gtc aac att gaa gtc tgg gtg gaa gca gag aat	688
Met Pro Thr Tyr Tyr Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn	
185 190 195 200	
gcc ctt ggg aag gtc tcc tca gag tct atc aat ttt gac ccc gtg gat	736
Ala Leu Gly Lys Val Ser Ser Glu Ser Ile Asn Phe Asp Pro Val Asp	
205 210 215	
aaa gtg aaa ccc acc cca cca tat aat tta tca gtg acc aac tca gaa	784
Lys Val Lys Pro Thr Pro Pro Tyr Asn Leu Ser Val Thr Asn Ser Glu	
220 225 230	
gaa tta tcc agt ata tta aag cta tca tgg gtc agt tca ggg ctg ggc	832
Glu Leu Ser Ser Ile Leu Lys Leu Ser Trp Val Ser Ser Gly Leu Gly	
235 240 245	
ggt ctt tta gat cta aag tct gac atc caa tat agg acc aaa gat gcc	880
Gly Leu Leu Asp Leu Lys Ser Asp Ile Gln Tyr Arg Thr Lys Asp Ala	
250 255 260	

tca act tgg atc cag gtc cct ctt gaa gat aca atg tct cct cga act	928
Ser Thr Trp Ile Gln Val Pro Leu Glu Asp Thr Met Ser Pro Arg Thr	
265 270 275 280	
tcc ttc act gtg cag gac ctc aag cct ttt aca gaa tat gtg ttt agg	976
Ser Phe Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg	
285 290 295	
atc cgg tcc att aag gac agt ggg aag ggc tac tgg agt gac tgg agt	1024
Ile Arg Ser Ile Lys Asp Ser Gly Lys Gly Tyr Trp Ser Asp Trp Ser	
300 305 310	
gag gag gct agt ggg acc aca tac gaa gac aga cca tcc aga cca cca	1072
Glu Glu Ala Ser Gly Thr Thr Tyr Glu Asp Arg Pro Ser Arg Pro Pro	
315 320 325	
agt ttc tgg tat aag aca aat cca tcc cat ggg cag gaa tat aga tct	1120
Ser Phe Trp Tyr Lys Thr Asn Pro Ser His Gly Gln Glu Tyr Arg Ser	
330 335 340	
gta cgg ctc ata tgg aag gca ctg cct ctt tct gaa gcc aat ggg aaa	1168
Val Arg Leu Ile Trp Lys Ala Leu Pro Leu Ser Glu Ala Asn Gly Lys	
345 350 355 360	
atc ttg gat tat gaa gtg att ctt acg cag tca aag tcc gtc tca caa	1216
Ile Leu Asp Tyr Glu Val Ile Leu Thr Gln Ser Lys Ser Val Ser Gln	
365 370 375	
acg tac aca gtc act ggc aca gag ctg acc gtg aat ctc acc aat gac	1264
Thr Tyr Thr Val Thr Gly Thr Glu Leu Thr Val Asn Leu Thr Asn Asp	
380 385 390	
cgc tat gtc gcg tct cta gca gca aga aac aag gtg ggc aaa tca gct	1312
Arg Tyr Val Ala Ser Leu Ala Ala Arg Asn Lys Val Gly Lys Ser Ala	
395 400 405	
gca gct gtc ctc acc atc ccc agc ccc cac gtc aca gct gct tat tct	1360
Ala Ala Val Leu Thr Ile Pro Ser Pro His Val Thr Ala Ala Tyr Ser	
410 415 420	
gta gtg aat ctt aaa gca ttt cca aaa gat aac ctg ctc tgg gtg gaa	1408
Val Val Asn Leu Lys Ala Phe Pro Lys Asp Asn Leu Leu Trp Val Glu	
425 430 435 440	
tgg aca cct cca cct aaa ccc gtg agc aag tac atc tta gag tgg tgt	1456
Trp Thr Pro Pro Pro Lys Pro Val Ser Lys Tyr Ile Leu Glu Trp Cys	
445 450 455	
gtg ttg tca gag aac gca ccc tgt gtt gaa gac tgg cag cag gaa gac	1504
Val Leu Ser Glu Asn Ala Pro Cys Val Glu Asp Trp Gln Gln Glu Asp	
460 465 470	
gct acc gtg aat cgg acc cac ttg aga gga cgc ctc ctg gag agc aag	1552
Ala Thr Val Asn Arg Thr His Leu Arg Gly Arg Leu Leu Glu Ser Lys	
475 480 485	
tgc tat caa atc aca gta act ccc gta ttc gcc acg ggg ccc gga ggc	1600

Cys	Tyr	Gln	Ile	Thr	Val	Thr	Pro	Val	Phe	Ala	Thr	Gly	Pro	Gly	Gly		
490						495					500						
tct	gag	tcc	ttg	aag	gcg	tac	ctc	aaa	caa	gcc	gct	cct	gcc	aga	gga	1648	
Ser	Glu	Ser	Leu	Lys	Ala	Tyr	Leu	Lys	Gln	Ala	Ala	Pro	Ala	Arg	Gly		
505					510					515					520		
ccg	act	gtt	cgg	aca	aag	aaa	gtg	ggg	aaa	aat	gaa	gct	gtc	tta	gcg	1696	
Pro	Thr	Val	Arg	Thr	Lys	Lys	Val	Gly	Lys	Asn	Glu	Ala	Val	Leu	Ala		
				525					530					535			
tgg	gac	cag	att	cct	gtg	gac	gac	cag	aat	ggc	ttc	att	aga	aac	tac	1744	
Trp	Asp	Gln	Ile	Pro	Val	Asp	Asp	Gln	Asn	Gly	Phe	Ile	Arg	Asn	Tyr		
			540					545					550				
tcc	ata	tct	tac	aga	acc	agc	gtg	gga	aag	gag	atg	gtt	gtg	cat	gtg	1792	
Ser	Ile	Ser	Tyr	Arg	Thr	Ser	Val	Gly	Lys	Glu	Met	Val	Val	His	Val		
		555					560					565					
gat	tct	tct	cac	acg	gag	tac	acg	ctg	tcc	tct	ctg	agt	agt	gat	acg	1840	
Asp	Ser	Ser	His	Thr	Glu	Tyr	Thr	Leu	Ser	Ser	Leu	Ser	Ser	Asp	Thr		
					570		575				580						
ttg	tac	atg	gtc	cga	atg	gcc	gcg	tac	aca	gat	gaa	ggg	ggg	aaa	gat	1888	
Leu	Tyr	Met	Val	Arg	Met	Ala	Ala	Tyr	Thr	Asp	Glu	Gly	Gly	Lys	Asp		
585					590					595					600		
ggg	ccg	gaa	ttc	act	ttt	aca	aca	cca	aag	ttc	gct	caa	gga	gaa	ata	1936	
Gly	Pro	Glu	Phe	Thr	Phe	Thr	Thr	Pro	Lys	Phe	Ala	Gln	Gly	Glu	Ile		
				605					610					615			
gaa	gcc	ata	gtc	gtg	cct	gtg	tgc	tta	gcc	ttc	ctc	ctg	aca	acc	ctg	1984	
Glu	Ala	Ile	Val	Val	Pro	Val	Cys	Leu	Ala	Phe	Leu	Leu	Thr	Thr	Leu		
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Leu	Gly	Val	Leu	Phe	Cys	Phe	Asn	Lys	Arg	Asp	Leu	Ile	Lys	Lys	His		
		635					640					645					
atc	tgg	cct	aat	gtt	cct	gat	cct	tcc	aag	agt	cat	att	gcc	cag	tgg	2080	
Ile	Trp	Pro	Asn	Val	Pro	Asp	Pro	Ser	Lys	Ser	His	Ile	Ala	Gln	Trp		
		650				655					660						
tca	cct	cac	acc	ccc	cca	agg	cac	aat	ttt	aac	tcc	aaa	gat	caa	atg	2128	
Ser	Pro	His	Thr	Pro	Pro	Arg	His	Asn	Phe	Asn	Ser	Lys	Asp	Gln	Met		
665					670					675					680		
tac	tcg	gac	ggc	aat	ttc	act	gat	gta	agc	gtt	gtg	gaa	ata	gaa	gca	2176	
Tyr	Ser	Asp	Gly	Asn	Phe	Thr	Asp	Val	Ser	Val	Val	Glu	Ile	Glu	Ala		
				685				690						695			
aac	aac	aag	aag	cct	tgt	cca	gat	gac	ctg	aag	tcc	gtg	gac	ctg	ttc	2224	
Asn	Asn	Lys	Lys	Pro	Cys	Pro	Asp	Asp	Leu	Lys	Ser	Val	Asp	Leu	Phe		
			700					705					710				
aag	aag	gag	aaa	gtg	agt	aca	gaa	ggg	cac	agc	agt	ggc	atc	ggg	ggc	2272	
Lys	Lys	Glu	Lys	Val	Ser	Thr	Glu	Gly	His	Ser	Ser	Gly	Ile	Gly	Gly		

715	720	725	
tct tca tgc atg tcc tcc tcc agg ccc agc atc tcc agc aac gag gag Ser Ser Cys Met Ser Ser Ser Arg Pro Ser Ile Ser Ser Asn Glu Glu 730 735 740			2320
aat gag tct gct cag agc acc gcc agc acg gtc gag tac tcc act gtg Asn Glu Ser Ala Gln Ser Thr Ala Ser Thr Val Glu Tyr Ser Thr Val 745 750 755 760			2368
gtg cac agc ggc tac agg cac cag gtc ccg tcc gtg caa gtg ttc tca Val His Ser Gly Tyr Arg His Gln Val Pro Ser Val Gln Val Phe Ser 765 770 775			2416
agg tcc gag tcc acc cag ccc ctg cta gac tcg gag gag cgg cca gaa Arg Ser Glu Ser Thr Gln Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu 780 785 790			2464
gac ctg cag ctg gtg gat agt gta gac ggt ggg gat gag atc ttg ccc Asp Leu Gln Leu Val Asp Ser Val Asp Gly Gly Asp Glu Ile Leu Pro 795 800 805			2512
agg caa ccg tat ttc aag cag aac tgc agt cag cct gaa gcc tgt cca Arg Gln Pro Tyr Phe Lys Gln Asn Cys Ser Gln Pro Glu Ala Cys Pro 810 815 820			2560
gag att tca cat ttt gaa agg tca aac cag gtt ttg tcc ggc aat gag Glu Ile Ser His Phe Glu Arg Ser Asn Gln Val Leu Ser Gly Asn Glu 825 830 835 840			2608
gag gat ttt gtc aga ctg aag cag cag cag gtt tca gat cac att tct Glu Asp Phe Val Arg Leu Lys Gln Gln Gln Val Ser Asp His Ile Ser 845 850 855			2656
cag ccc tat gga tcc gag caa cgg agg ctg ttt cag gaa ggc tct aca Gln Pro Tyr Gly Ser Glu Gln Arg Arg Leu Phe Gln Glu Gly Ser Thr 860 865 870			2704
gcg gat gct ctt ggc acg ggg gct gat gga cag atg gag aga ttt gaa Ala Asp Ala Leu Gly Thr Gly Ala Asp Gly Gln Met Glu Arg Phe Glu 875 880 885			2752
tct gtt gga atg gag acc aca att gat gaa gaa att ccc aaa agt tac Ser Val Gly Met Glu Thr Thr Ile Asp Glu Glu Ile Pro Lys Ser Tyr 890 895 900			2800
ttg cca cag act gta aga caa ggt ggc tac atg ccg cag tgaaggactg Leu Pro Gln Thr Val Arg Gln Gly Gly Tyr Met Pro Gln 905 910 915			2849
gctcctgaac ttcagcagga actgcaaaat aaagctaaag acgagtggct tcagatgaga			2909
aacagtcctc actccctgaa gataggcatt gcctctaagg acaaagtcac acctgggccc			2969
tctccattcc agagtagctg gaattc			2995

<211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "mgp1", an artificially synthesized primer sequence

<400> 18
 cccaagcttg aattcacttt tacaaca

27

<210> 19
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "mgp3", an artificially synthesized primer sequence

<400> 19
 tttgcggccg cgaattccag ctactctgg

29

<210> 20
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "mgp2", an artificially synthesized primer sequence

<400> 20
 cccaagcttg aattcaaaaa acacatctgg ctt

33

<210> 21
 <211> 1662
 <212> DNA
 <213> Artificial Sequence

<220>

<221> CDS

<222> (11)..(1648)

<220>

<223> Description of Artificial Sequence: "hPM1-BvGS3 ", a designed single chain Fv gene sequence

<400> 21
 gaattccacc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca 49
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr
 1 5 10

gct aca ggt gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt 97
 Ala Thr Gly Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly
 15 20 25

ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc	145
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly	
30 35 40 45	
tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct	193
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro	
50 55 60	
gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca	241
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr	
65 70 75	
acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc	289
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr	
80 85 90	
agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac	337
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp	
95 100 105	
acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg	385
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met	
110 115 120 125	
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt	433
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly	
130 135 140	
ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg	481
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met	
145 150 155	
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc	529
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr	
160 165 170	
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac	577
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr	
175 180 185	
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc	625
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser	
190 195 200 205	
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt	673
Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly	
210 215 220	
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct	721
Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala	
225 230 235	
acc tac tac tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa	769
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln	
240 245 250	
ggg acc aag gtg gaa atc aaa tct aga ggt ggt ggt ggt tcg ggt ggt	817

Gly	Thr	Lys	Val	Glu	Ile	Lys	Ser	Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly		
255						260					265						
ggg	ggg	tcg	ggg	ggg	ggc	gga	tcg	gtc	gac	tcc	cag	gtc	caa	ctg	cag	865	
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Val	Asp	Ser	Gln	Val	Gln	Leu	Gln		
270				275					280					285			
gag	agc	ggg	cca	ggg	ctt	gtg	aga	cct	agc	cag	acc	ctg	agc	ctg	acc	913	
Glu	Ser	Gly	Pro	Gly	Leu	Val	Arg	Pro	Ser	Gln	Thr	Leu	Ser	Leu	Thr		
			290					295						300			
tgc	acc	gtg	tct	ggc	tac	tca	att	acc	agc	gat	cat	gcc	tgg	agc	tgg	961	
Cys	Thr	Val	Ser	Gly	Tyr	Ser	Ile	Thr	Ser	Asp	His	Ala	Trp	Ser	Trp		
		305					310					315					
gtt	cgc	cag	cca	cct	gga	cga	ggg	ctt	gag	tgg	att	gga	tac	att	agt	1009	
Val	Arg	Gln	Pro	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Ser		
		320					325					330					
tat	agt	gga	atc	aca	acc	tat	aat	cca	tct	ctc	aaa	tcc	aga	gtg	aca	1057	
Tyr	Ser	Gly	Ile	Thr	Thr	Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr		
	335					340					345						
atg	ctg	aga	gac	acc	agc	aag	aac	cag	ttc	agc	ctg	aga	ctc	agc	agc	1105	
Met	Leu	Arg	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu	Arg	Leu	Ser	Ser		
350				355				360						365			
gtg	aca	gcc	gcc	gac	acc	gcg	gtt	tat	tat	tgt	gca	aga	tcc	cta	gct	1153	
Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Leu	Ala		
			370					375						380			
cgg	act	acg	gct	atg	gac	tac	tgg	ggg	caa	ggc	agc	ctc	gtc	aca	gtc	1201	
Arg	Thr	Thr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Ser	Leu	Val	Thr	Val		
			385				390						395				
tcc	tca	ggg	ggg	ggg	ggg	tcg	ggg	ggg	ggg	ggg	tcg	ggg	ggg	ggc	gga	1249	
Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly		
		400				405					410						
tcg	gac	atc	cag	atg	acc	cag	agc	cca	agc	agc	ctg	agc	gcc	agc	gtg	1297	
Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val		
	415					420					425						
ggg	gac	aga	gtg	acc	atc	acc	tgt	aga	gcc	agc	cag	gac	atc	agc	agt	1345	
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Ser	Ser		
430				435				440					445				
tac	ctg	aat	tgg	tac	cag	cag	aag	cca	gga	aag	gct	cca	aag	ctg	ctg	1393	
Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu		
			450					455					460				
atc	tac	tac	acc	tcc	aga	ctg	cac	tct	ggg	gtg	cca	agc	aga	ttc	agc	1441	
Ile	Tyr	Tyr	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser		
			465				470						475				
ggg	agc	ggg	agc	ggg	acc	gac	ttc	acc	ttc	acc	atc	agc	agc	ctc	cag	1489	
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln		

480	485	490	
cca gag gac atc gct acc tac tac tgc caa cag ggt aac acg ctt cca			1537
Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro			
495	500	505	
tac acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct			1585
Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala			
510	515	520	525
gca cca tct gtc ttc atc ttc ccg cca tct gat aag ctt gac tac aaa			1633
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Lys Leu Asp Tyr Lys			
	530	535	540
gac gat gac gat aaa taataagcgg ccgc			1662
Asp Asp Asp Asp Lys			
	545		

<210> 22

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "BvGS3", an artificially synthesized primer sequence

<400> 22

ggagtcgacc gatccgccac caccogaacc accaccaccc gaaccaccac cacctttgat 60

ttccaccttg gt

72

<210> 23

<211> 780

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(780)

<220>

<223> Description of Artificial Sequence: "shPM1(Δ EL)", a designed single chain Fv gene sequence

<400> 23

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1

5

10

15

gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96

Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg

20

25

30

cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att 144

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile

35

40

45

acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt	192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly	
50 55 60	
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat	240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn	
65 70 75 80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac	288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn	
85 90 95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg	384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp	
115 120 125	
ggc caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tgc ggt	432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
130 135 140	
ggc ggt ggt tgc ggt ggt ggc gga tgc gac atc cag atg acc cag agc	480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
145 150 155 160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt	528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys	
165 170 175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag	576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	
180 185 190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His	
195 200 205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc	672
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
210 215 220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac	720
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr	
225 230 235 240	
tgc caa cag gga aat act tta cca tac acg ttc ggc caa ggg acc aag	768
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
245 250 255	
gtg gaa atc aaa	780
Val Glu Ile Lys	
260	

<210> 24
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(321)

<400> 24
 cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag 48
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 1 5 10 15
 cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 96
 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 20 25 30
 tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 144
 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 35 40 45
 tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 192
 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 50 55 60
 acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 240
 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 65 70 75 80
 aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 288
 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 85 90 95
 ccc gtc aca aag agc ttc aac agg gga gag tct 321
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Ser
 100 105

<210> 25
 <211> 363
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(363)

<400> 25
 gtg gcc ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag 48
 Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu
 1 5 10 15
 cag ctg aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc 96
 Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly
 20 25 30

ttc tct ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc 144
 Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro
 35 40 45

ttg tcc ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag 192
Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln
50 55 60

gcc cca ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag 240
Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu
65 70 75 80

gaa tgg aac acg ggg gag acc tac acc tgc gtg gcc cat gag gcc ctg 288
Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Ala His Glu Ala Leu
85 90 95

ccc aac agg gtc acc gag agg acc gtg gac aag tcc acc gag ggg gag 336
Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Glu Gly Glu
100 105 110

gtg agc gcc gac gag gag ggc ttt gag 363
Val Ser Ala Asp Glu Glu Gly Phe Glu
115 120

<210> 26

<211> 1101

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) .. (1101)

<220>

<223> Description of Artificial Sequence: "shPM1-Kappa", a designed single chain Fv gene sequence

<400> 26

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
20 25 30

cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att 144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile
35 40 45

acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt 192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly
50 55 60

ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat	240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn	
65 70 75 80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac	288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn	
85 90 95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg	384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp	
115 120 125	
ggg caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tgc ggt	432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
130 135 140	
ggg ggt ggt tgc ggt ggt ggc gga tgc gac atc cag atg acc cag agc	480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
145 150 155 160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt	528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys	
165 170 175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag	576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	
180 185 190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His	
195 200 205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc	672
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
210 215 220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac	720
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr	
225 230 235 240	
tgc caa cag gga aat act tta cca tac acg ttc ggc caa ggg acc aag	768
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
245 250 255	
gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg	816
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
260 265 270	
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg	864
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
275 280 285	
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat	912

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 290 295 300

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac 960
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 305 310 315 320

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa 1008
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 325 330 335

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 1056
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 340 345 350

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tct 1101
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Ser
 355 360 365

<210> 27

<211> 1143

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1143)

<220>

<223> Description of Artificial Sequence: "shPM1-MCH4", a designed single chain Fv gene sequence

<400> 27

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96
 Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
 20 25 30

cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att 144
 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile
 35 40 45

acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt 192
 Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly
 50 55 60

ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat 240
 Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn
 65 70 75 80

cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac 288
 Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn

					85						90						95					
cag	ttc	agc	ctg	aga	ctc	agc	agc	gtg	aca	gcc	gcc	gac	acc	gcg	gtt	336						
Gln	Phe	Ser	Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val							
					100						105						110					
tat	tat	tgt	gca	aga	tcc	cta	gct	cgg	act	acg	gct	atg	gac	tac	tgg	384						
Tyr	Tyr	Cys	Ala	Arg	Ser	Leu	Ala	Arg	Thr	Thr	Ala	Met	Asp	Tyr	Trp							
					115						120						125					
ggc	caa	ggc	agc	ctc	gtc	aca	gtc	tcc	tca	ggc	ggc	ggc	ggc	tcg	ggc	432						
Gly	Gln	Gly	Ser	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly							
					130						135						140					
ggc	ggc	ggc	tcg	ggc	ggc	ggc	gga	tcg	gac	atc	cag	atg	acc	cag	agc	480						
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser							
					145						155						160					
cca	agc	agc	ctg	agc	gcc	agc	gtg	ggc	gac	aga	gtg	acc	atc	acc	tgt	528						
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys							
					165						170						175					
aga	gcc	agc	cag	gac	atc	agc	agt	tac	ctg	aat	tgg	tac	cag	cag	aag	576						
Arg	Ala	Ser	Gln	Asp	Ile	Ser	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys							
					180						185						190					
cca	gga	aag	gct	cca	aag	ctg	ctg	atc	tac	tac	acc	tcc	aga	ctg	cac	624						
Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	Arg	Leu	His							
					195						200						205					
tct	ggc	gtg	cca	agc	aga	ttc	agc	ggc	agc	ggc	agc	ggc	acc	gac	ttc	672						
Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe							
					210						215						220					
acc	ttc	acc	atc	agc	agc	ctc	cag	cca	gag	gac	atc	gct	acc	tac	tac	720						
Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr							
					225						235						240					
tgc	caa	cag	gga	aat	act	tta	cca	tac	acg	ttc	ggc	caa	ggg	acc	aag	768						
Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys							
					245						250						255					
gtg	gaa	atc	aaa	gtg	gcc	ctg	cac	agg	ccc	gat	gtc	tac	ttg	ctg	cca	816						
Val	Glu	Ile	Lys	Val	Ala	Leu	His	Arg	Pro	Asp	Val	Tyr	Leu	Leu	Pro							
					260						265						270					
cca	gcc	cgg	gag	cag	ctg	aac	ctg	cgg	gag	tcg	gcc	acc	atc	acg	tgc	864						
Pro	Ala	Arg	Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Ile	Thr	Cys							
					275						280						285					
ctg	gtg	acg	ggc	ttc	tct	ccc	gcg	gac	gtc	ttc	gtg	cag	tgg	atg	cag	912						
Leu	Val	Thr	Gly	Phe	Ser	Pro	Ala	Asp	Val	Phe	Val	Gln	Trp	Met	Gln							
					290						295						300					
agg	ggg	cag	ccc	ttg	tcc	ccg	gag	aag	tat	gtg	acc	agc	gcc	cca	atg	960						
Arg	Gly	Gln	Pro	Leu	Ser	Pro	Glu	Lys	Tyr	Val	Thr	Ser	Ala	Pro	Met							
					305						310						315					

cct gag ccc cag gcc cca ggc cgg tac ttc gcc cac agc atc ctg acc 1008
 Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr
 325 330 335

gtg tcc gaa gag gaa tgg aac acg ggg gag acc tac acc tgc gtg gcc 1056
 Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Ala
 340 345 350

cat gag gcc ctg ccc aac agg gtc acc gag agg acc gtg gac aag tcc 1104
 His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser
 355 360 365

acc gag ggg gag gtg agc gcc gac gag gag ggc ttt gag 1143
 Thr Glu Gly Glu Val Ser Ala Asp Glu Glu Gly Phe Glu
 370 375 380

<210> 28
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "EF-1", an artificially synthesized primer sequence

<400> 28
 cagacagtgg ttcaaagt 18

<210> 29
 <211> 107
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "SCP-C2", an artificially synthesized primer sequence

<400> 29
 aaagcggccg cttattatatt atcgatcatg tctttgtagt ctgaagcttt gatttccacc 60
 ttgggtccctt ggccgaacgt gtatggtaaa gtatttccct gttggca 107

<210> 30
 <211> 1557
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1557)
 <220>

<223> Description of Artificial Sequence: "shPM1(Δ EL)-BvGS3", a designed single chain Fv gene sequence

<400> 30

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga	96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
20 25 30	
cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att	144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile	
35 40 45	
acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt	192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly	
50 55 60	
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat	240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn	
65 70 75 80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac	288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn	
85 90 95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg	384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp	
115 120 125	
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt	432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
130 135 140	
ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc	480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
145 150 155 160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt	528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys	
165 170 175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag	576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	
180 185 190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His	
195 200 205	

tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe 210 215 220	672
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr 225 230 235 240	720
tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys 245 250 255	768
gtg gaa atc aaa ggt ggt ggt ggt tgc ggt ggt ggt ggt tgc ggt ggt Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly 260 265 270	816
ggc gga tgc gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly 275 280 285	864
ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly 290 295 300	912
tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro 305 310 315 320	960
gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr 325 330 335	1008
acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr 340 345 350	1056
agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp 355 360 365	1104
acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met 370 375 380	1152
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly 385 390 395 400	1200
ggt tgc ggt ggt ggt ggt tgc ggt ggt ggc gga tgc gac atc cag atg Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met 405 410 415	1248
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr 420 425 430	1296
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac	1344

Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr
 435 440 445

cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc 1392
 Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser
 450 455 460

aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt 1440
 Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
 465 470 475 480

acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct 1488
 Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
 485 490 495

acc tac tac tgc caa cag gga aat act tta cca tac acg ttc ggc caa 1536
 Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln
 500 505 510

ggg acc aag gtg gaa atc aaa 1557
 Gly Thr Lys Val Glu Ile Lys
 515

<210> 31

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "Kappal", an artificially synthesized primer sequence

<400> 31

ccgccatctg atgagcagtt gaaatctgg 29

<210> 32

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "Kappa2", an artificially synthesized primer sequence

<400> 32

ttatttatcg tcatcgctctt tgtagtcaag cttagactct cccctgttga agct 54

<210> 33

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "SCP-K", an artificially synthesized primer sequence

<400> 33

ttcaactgct catcagatgg cgggaagat

29

<210> 34

<211> 1878

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1878)

<220>

<223> Description of Artificial Sequence: "shPM1-Kappa-BvGS3", a designed single chain Fv gene sequence

<400> 34

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
20 25 30

cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att 144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile
35 40 45

acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt 192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly
50 55 60

ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat 240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn
65 70 75 80

cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac 288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn
85 90 95

cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt 336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
100 105 110

tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg 384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp
115 120 125

ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tgg ggt 432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
130 135 140

ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc	480
Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
145 150 155 160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt	528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys	
165 170 175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag	576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	
180 185 190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His	
195 200 205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc	672
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
210 215 220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac	720
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr	
225 230 235 240	
tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag	768
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
245 250 255	
gtg gaa atc aaa ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt	816
Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
260 265 270	
ggc gga tcg gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt	864
Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly	
275 280 285	
ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc	912
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly	
290 295 300	
tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct	960
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro	
305 310 315 320	
gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca	1008
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr	
325 330 335	
acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc	1056
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr	
340 345 350	
agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac	1104
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp	
355 360 365	

acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg	1152
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met	
370 375 380	
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt	1200
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly	
385 390 395 400	
ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg	1248
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln Met	
405 410 415	
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc	1296
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr	
420 425 430	
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac	1344
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr	
435 440 445	
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc	1392
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser	
450 455 460	
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt	1440
Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly	
465 470 475 480	
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct	1488
Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala	
485 490 495	
acc tac tac tgc caa cag gga aat act tta cca tac acg ttc ggc caa	1536
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln	
500 505 510	
ggg acc aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc	1584
Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe	
515 520 525	
atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt	1632
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val	
530 535 540	
gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg	1680
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp	
545 550 555 560	
aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca	1728
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr	
565 570 575	
gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg	1776
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr	
580 585 590	
ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc	1824

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 595 600 605

acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga 1872
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 610 615 620

gag tct 1878
 Glu Ser
 625

<210> 35
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "MCH4-1", an artificially synthesized primer sequence

<400> 35
 gtggaaatca aagtggccct gcacaggcc 29

<210> 36
 <211> 68
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "MCH4-2.1", an artificially synthesized primer sequence

<400> 36
 tagtcaagct tctcaaattc ctcttcgtcg gcgctaacct ctccttcggt ggacttgctc 60
 acggtcct 68

<210> 37
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: "SCP-Mu", an artificially synthesized primer sequence

<400> 37
 tgcagggcca ctttgatttc caccttggt 29

<210> 38
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "MCH4-2.2", an artificially synthesized primer sequence

<400> 38

aaagcggccg cttattattt atcgtcatcg tctttgtagt caagcttctc aaa 53

<210> 39

<211> 1920

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1920)

<220>

<223> Description of Artificial Sequence: "shPM1-MCH4-BvGS3", a designed single chain Fv gene sequence

<400> 39

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga	96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
20 25 30	
cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att	144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile	
35 40 45	
acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt	192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly	
50 55 60	
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat	240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn	
65 70 75 80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac	288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn	
85 90 95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg	384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp	
115 120 125	
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tgg ggt	432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
130 135 140	

ggt ggt ggt tct ggt ggt ggc gga tct gac atc cag atg acc cag agc 480
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser 160
 145 150 155

cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt 528
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys 175
 165 170

aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag 576
 Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys 190
 180 185

cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac 624
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His 205
 195 200

tct ggt gtg cca agc aga ttc agc ggt agc ggt acc gac ttc 672
 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe 220
 210 215

acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac 720
 Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr 240
 225 230 235

tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag 768
 Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys 255
 245 250

gtg gaa atc aaa ggt ggt ggt ggt tct ggt ggt ggt ggt tct ggt ggt 816
 Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly 270
 260 265

ggc gga tct gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt 864
 Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly 285
 275 280

ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc 912
 Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly 300
 290 295

tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct 960
 Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro 320
 305 310 315

gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca 1008
 Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr 335
 325 330

acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc 1056
 Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr 350
 340 345

agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac 1104
 Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp 365
 355 360

acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg	1152
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met	
370 375 380	
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt	1200
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly	
385 390 395 400	
ggg tgc ggt ggt ggt ggt tgc ggt ggt ggc gga tgc gac atc cag atg	1248
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met	
405 410 415	
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc	1296
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr	
420 425 430	
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac	1344
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr	
435 440 445	
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc	1392
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser	
450 455 460	
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt	1440
Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly	
465 470 475 480	
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct	1488
Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala	
485 490 495	
acc tac tac tgc caa cag gga aat act tta cca tac acg ttc ggc caa	1536
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln	
500 505 510	
ggg acc aag gtg gaa atc aaa gtg gcc ctg cac agg ccc gat gtc tac	1584
Gly Thr Lys Val Glu Ile Lys Val Ala Leu His Arg Pro Asp Val Tyr	
515 520 525	
ttg ctg cca cca gcc cgg gag cag ctg aac ctg cgc gag tgc gcc acc	1632
Leu Leu Pro Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr	
530 535 540	
atc acg tgc ctg gtg acg ggc ttc tct ccc gcg gac gtc ttc gtg cag	1680
Ile Thr Cys Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln	
545 550 555 560	
tgg atg cag agg ggg cag ccc ttg tcc ccg gag aag tat gtg acc agc	1728
Trp Met Gln Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser	
565 570 575	
gcc cca atg cct gag ccc cag gcc cca ggc cgg tac ttc gcc cac agc	1776
Ala Pro Met Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser	
580 585 590	
atc ctg acc gtg tcc gaa gag gaa tgg aac acg ggg gag acc tac acc	1824

Ile Leu Thr Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr
595 600 605

tgc gtg gcc cat gag gcc ctg ccc aac agg gtc acc gag agg acc gtg 1872
 Cys Val Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val
 610 615 620

gac aag tcc acc gag ggg gag gtg agc gcc gac gag gag ggc ttt gag 1920
Asp Lys Ser Thr Glu Gly Glu Val Ser Ala Asp Glu Glu Gly Phe Glu
625 630 635 640